

## SEQUENCE LISTING

<110> GALLOWAY, DARREL R.  
MATECZUN, ALFRED J.

<120> METHODS FOR PROTECTION AGAINST LETHAL INFECTION WITH  
BACILLUS ANTHRACIS

<130> 22727-04079

<140> 09/747,521

<141> 2000-12-21

<150> 60/171,459

<151> 1999-12-22

<160> 10

<170> PatentIn Ver. 3.3

<210> 1

<211> 2430

<212> DNA

<213> Bacillus anthracis

<220>

<221> CDS

<222> (1) .. (2427)

<400> 1

atg aat ata aaa aaa gaa ttt ata aaa gta att agt atg tca tgt tta	48
Met Asn Ile Lys Lys Glu Phe Ile Lys Val Ile Ser Met Ser Cys Leu	
1 5 10 15	
gta aca gca att act ttg agt ggt ccc gtc ttt atc ccc ctt gta cag	96
Val Thr Ala Ile Thr Leu Ser Gly Pro Val Phe Ile Pro Leu Val Gln	
20 25 30	
ggg gcg ggc ggt cat ggt gat gta ggt atg cac gta aaa gag aaa gag	144
Gly Ala Gly Gly His Gly Asp Val Gly Met His Val Lys Glu Lys Glu	
35 40 45	
aaa aat aaa gat gag aat aag aga aaa gat gaa gaa cga aat aaa aca	192
Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp Glu Glu Arg Asn Lys Thr	
50 55 60	
cag gaa gag cat tta aag gaa atc atg aaa cac att gta aaa ata gaa	240
Gln Glu Glu His Leu Lys Glu Ile Met Lys His Ile Val Lys Ile Glu	
65 70 75 80	
gta aaa ggg gag gaa gct gtt aaa aaa gag gca gca gaa aag cta ctt	288
Val Lys Gly Glu Glu Ala Val Lys Lys Glu Ala Ala Glu Lys Leu Leu	
85 90 95	
gag aaa gta cca tct gat gtt tta gag atg tat aaa gca att gga gga	336
Glu Lys Val Pro Ser Asp Val Leu Glu Met Tyr Lys Ala Ile Gly Gly	
100 105 110	

aag ata tat att gtg gat ggt gat att aca aaa cat ata tct tta gaa Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr Lys His Ile Ser Leu Glu 115 120 125	384
gca tta tct gaa gat aag aaa aaa ata aaa gac att tat ggg aaa gat Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys Asp Ile Tyr Gly Lys Asp 130 135 140	432
gct tta tta cat gaa cat tat gta tat gca aaa gaa gga tat gaa ccc Ala Leu Leu His Glu His Tyr Val Tyr Ala Lys Glu Gly Tyr Glu Pro 145 150 155 160	480
gta ctt gta atc caa tct tcg gaa gat tat gta gaa aat act gaa aag Val Leu Val Ile Gln Ser Ser Glu Asp Tyr Val Glu Asn Thr Glu Lys 165 170 175	528
gca ctg aac gtt tat tat gaa ata ggt aag ata tta tca agg gat att Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys Ile Leu Ser Arg Asp Ile 180 185 190	576
tta agt aaa att aat caa cca tat cag aaa ttt tta gat gta tta aat Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys Phe Leu Asp Val Leu Asn 195 200 205	624
acc att aaa aat gca tct gat tca gat gga caa gat ctt tta ttt act Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly Gln Asp Leu Leu Phe Thr 210 215 220	672
aat cag ctt aag gaa cat ccc aca gac ttt tct gta gaa ttc ttg gaa Asn Gln Leu Lys Glu His Pro Thr Asp Phe Ser Val Glu Phe Leu Glu 225 230 235 240	720
caa aat agc aat gag gta caa gaa gta ttt gcg aaa gct ttt gca tat Gln Asn Ser Asn Glu Val Gln Glu Val Phe Ala Lys Ala Phe Ala Tyr 245 250 255	768
tat atc gag cca cag cat cgt gat gtt tta cag ctt tat gca ccg gaa Tyr Ile Glu Pro Gln His Arg Asp Val Leu Gln Leu Tyr Ala Pro Glu 260 265 270	816
gct ttt aat tac atg gat aaa ttt aac gaa caa gaa ata aat cta tcc Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu Gln Glu Ile Asn Leu Ser 275 280 285	864
ttg gaa gaa ctt aaa gat caa cgg atg ctg tca aga tat gaa aaa tgg Leu Glu Glu Leu Lys Asp Gln Arg Met Leu Ser Arg Tyr Glu Lys Trp 290 295 300	912
gaa aag ata aaa cag cac tat caa cac tgg agc gat tct tta tct gaa Glu Lys Ile Lys Gln His Tyr Gln His Trp Ser Asp Ser Leu Ser Glu 305 310 315 320	960
gaa gga aga gga ctt tta aaa aag ctg cag att cct att gag cca aag Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln Ile Pro Ile Glu Pro Lys 325 330 335	1008

aaa gat gac ata att cat tct tta tct caa gaa gaa aaa gag ctt cta	1056
Lys Asp Asp Ile Ile His Ser Ser Leu Ser Gln Glu Glu Lys Glu Leu Leu	
340 345 350	
aaa aga ata caa att gat agt agt gat ttt tta tct act gag gaa aaa	1104
Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe Leu Ser Thr Glu Glu Lys	
355 360 365	
gag ttt tta aaa aag cta caa att gat att cgt gat tct tta tct gaa	1152
Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile Arg Asp Ser Leu Ser Glu	
370 375 380	
gaa gaa aaa gag ctt tta aat aga ata cag gtg gat agt agt aat cct	1200
Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln Val Asp Ser Ser Asn Pro	
385 390 395 400	
tta tct gaa aaa gaa aaa gag ttt tta aaa aag ctg aaa ctt gat att	1248
Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys Lys Leu Lys Leu Asp Ile	
405 410 415	
caa cca tat gat att aat caa agg ttg caa gat aca gga ggg tta att	1296
Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln Asp Thr Gly Gly Leu Ile	
420 425 430	
gat agt ccg tca att aat ctt gat gta aga aag cag tat aaa agg gat	1344
Asp Ser Pro Ser Ile Asn Leu Asp Val Arg Lys Gln Tyr Lys Arg Asp	
435 440 445	
att caa aat att gat gct tta tta cat caa tcc att gga agt acc ttg	1392
Ile Gln Asn Ile Asp Ala Leu Leu His Gln Ser Ile Gly Ser Thr Leu	
450 455 460	
tac aat aaa att tat ttg tat gaa aat atg aat atc aat aac ctt aca	1440
Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met Asn Ile Asn Asn Leu Thr	
465 470 475 480	
gca acc cta ggt gcg gat tta gtt gat tcc act gat aat act aaa att	1488
Ala Thr Leu Gly Ala Asp Leu Val Asp Ser Thr Asp Asn Thr Lys Ile	
485 490 495	
aat aga ggt att ttc aat gaa ttc aaa aaa aat ttc aaa tat agt att	1536
Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys Asn Phe Lys Tyr Ser Ile	
500 505 510	
tct agt aac tat atg att gtt gat ata aat gaa agg cct gca tta gat	1584
Ser Ser Asn Tyr Met Ile Val Asp Ile Asn Glu Arg Pro Ala Leu Asp	
515 520 525	
aat gag cgt ttg aaa tgg aga atc caa tta tca cca gat act cga gca	1632
Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu Ser Pro Asp Thr Arg Ala	
530 535 540	
gga tat tta gaa aat gga aag ctt ata tta caa aga aac atc ggt ctg	1680
Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu Gln Arg Asn Ile Gly Leu	
545 550 555 560	

gaa ata aag gat gta caa ata att aag caa tcc gaa aaa gaa tat ata Glu Ile Lys Asp Val Gln Ile Ile Lys Gln Ser Glu Lys Glu Tyr Ile 565 570 575	1728
agg att gat gcg aaa gta gtg cca aag agt aaa ata gat aca aaa att Arg Ile Asp Ala Lys Val Val Pro Lys Ser Lys Ile Asp Thr Lys Ile 580 585 590	1776
caa gaa gca cag tta aat ata aat cag gaa tgg aat aaa gca tta ggg Gln Glu Ala Gln Leu Asn Ile Asn Gln Glu Trp Asn Lys Ala Leu Gly 595 600 605	1824
tta cca aaa tat aca aag ctt att aca ttc aac gtg cat aat aga tat Leu Pro Lys Tyr Thr Lys Leu Ile Thr Phe Asn Val His Asn Arg Tyr 610 615 620	1872
gca tcc aat att gta gaa agt gct tat tta ata ttg aat gaa tgg aaa Ala Ser Asn Ile Val Glu Ser Ala Tyr Leu Ile Leu Asn Glu Trp Lys 625 630 635 640	1920
aat aat att caa agt gat ctt ata aaa aag gta aca aat tac tta gtt Asn Asn Ile Gln Ser Asp Leu Ile Lys Lys Val Thr Asn Tyr Leu Val 645 650 655	1968
gat ggt aat gga aga ttt gtt ttt acc gat att act ctc cct aat ata Asp Gly Asn Gly Arg Phe Val Phe Thr Asp Ile Thr Leu Pro Asn Ile 660 665 670	2016
gct gaa caa tat aca cat caa gat gag ata tat gag caa gtt cat tca Ala Glu Gln Tyr Thr His Gln Asp Glu Ile Tyr Glu Gln Val His Ser 675 680 685	2064
aaa ggg tta tat gtt cca gaa tcc cgt tct ata tta ctc cat gga cct Lys Gly Leu Tyr Val Pro Glu Ser Arg Ser Ile Leu Leu His Gly Pro 690 695 700	2112
tca aaa ggt gta gaa tta agg aat gat agt gag ggt ttt ata cac gaa Ser Lys Gly Val Glu Leu Arg Asn Asp Ser Glu Gly Phe Ile His Glu 705 710 715 720	2160
ttt gga cat gct gtg gat gat tat gct gga tat cta tta gat aag aac Phe Gly His Ala Val Asp Asp Tyr Ala Gly Tyr Leu Leu Asp Lys Asn 725 730 735	2208
caa tct gat tta gtt aca aat tct aaa aaa ttc att gat att ttt aag Gln Ser Asp Leu Val Thr Asn Ser Lys Lys Phe Ile Asp Ile Phe Lys 740 745 750	2256
gaa gaa ggg agt aat tta act tcg tat ggg aga aca aat gaa gcg gaa Glu Glu Gly Ser Asn Leu Thr Ser Tyr Gly Arg Thr Asn Glu Ala Glu 755 760 765	2304
ttt ttt gca gaa gcc ttt agg tta atg cat tct acg gac cat gct gaa Phe Phe Ala Glu Ala Phe Arg Leu Met His Ser Thr Asp His Ala Glu 770 775 780	2352

cgt tta aaa gtt caa aaa aat gct ccg aaa act ttc caa ttt att aac 2400  
 Arg Leu Lys Val Gln Lys Asn Ala Pro Lys Thr Phe Gln Phe Ile Asn  
 785 790 795 800

gat cag att aag ttc att att aac tca taa 2430  
 Asp Gln Ile Lys Phe Ile Ile Asn Ser  
 805

<210> 2  
 <211> 809  
 <212> PRT  
 <213> Bacillus anthracis

<400> 2  
 Met Asn Ile Lys Lys Glu Phe Ile Lys Val Ile Ser Met Ser Cys Leu  
 1 5 10 15  
 Val Thr Ala Ile Thr Leu Ser Gly Pro Val Phe Ile Pro Leu Val Gln  
 20 25 30  
 Gly Ala Gly Gly His Gly Asp Val Gly Met His Val Lys Glu Lys Glu  
 35 40 45  
 Lys Asn Lys Asp Glu Asn Lys Arg Lys Asp Glu Glu Arg Asn Lys Thr  
 50 55 60  
 Gln Glu Glu His Leu Lys Glu Ile Met Lys His Ile Val Lys Ile Glu  
 65 70 75 80  
 Val Lys Gly Glu Glu Ala Val Lys Lys Glu Ala Ala Glu Lys Leu Leu  
 85 90 95  
 Glu Lys Val Pro Ser Asp Val Leu Glu Met Tyr Lys Ala Ile Gly Gly  
 100 105 110  
 Lys Ile Tyr Ile Val Asp Gly Asp Ile Thr Lys His Ile Ser Leu Glu  
 115 120 125  
 Ala Leu Ser Glu Asp Lys Lys Lys Ile Lys Asp Ile Tyr Gly Lys Asp  
 130 135 140  
 Ala Leu Leu His Glu His Tyr Val Tyr Ala Lys Glu Gly Tyr Glu Pro  
 145 150 155 160  
 Val Leu Val Ile Gln Ser Ser Glu Asp Tyr Val Glu Asn Thr Glu Lys  
 165 170 175  
 Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys Ile Leu Ser Arg Asp Ile  
 180 185 190  
 Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys Phe Leu Asp Val Leu Asn  
 195 200 205  
 Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly Gln Asp Leu Leu Phe Thr  
 210 215 220

Asn Gln Leu Lys Glu His Pro Thr Asp Phe Ser Val Glu Phe Leu Glu  
 225 230 235 240  
 Gln Asn Ser Asn Glu Val Gln Glu Val Phe Ala Lys Ala Phe Ala Tyr  
 245 250 255  
 Tyr Ile Glu Pro Gln His Arg Asp Val Leu Gln Leu Tyr Ala Pro Glu  
 260 265 270  
 Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu Gln Glu Ile Asn Leu Ser  
 275 280 285  
 Leu Glu Glu Leu Lys Asp Gln Arg Met Leu Ser Arg Tyr Glu Lys Trp  
 290 295 300  
 Glu Lys Ile Lys Gln His Tyr Gln His Trp Ser Asp Ser Leu Ser Glu  
 305 310 315 320  
 Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln Ile Pro Ile Glu Pro Lys  
 325 330 335  
 Lys Asp Asp Ile Ile His Ser Leu Ser Gln Glu Glu Lys Glu Leu Leu  
 340 345 350  
 Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe Leu Ser Thr Glu Glu Lys  
 355 360 365  
 Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile Arg Asp Ser Leu Ser Glu  
 370 375 380  
 Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln Val Asp Ser Ser Asn Pro  
 385 390 395 400  
 Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys Lys Leu Lys Leu Asp Ile  
 405 410 415  
 Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln Asp Thr Gly Gly Leu Ile  
 420 425 430  
 Asp Ser Pro Ser Ile Asn Leu Asp Val Arg Lys Gln Tyr Lys Arg Asp  
 435 440 445  
 Ile Gln Asn Ile Asp Ala Leu Leu His Gln Ser Ile Gly Ser Thr Leu  
 450 455 460  
 Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met Asn Ile Asn Asn Leu Thr  
 465 470 475 480  
 Ala Thr Leu Gly Ala Asp Leu Val Asp Ser Thr Asp Asn Thr Lys Ile  
 485 490 495  
 Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys Asn Phe Lys Tyr Ser Ile  
 500 505 510  
 Ser Ser Asn Tyr Met Ile Val Asp Ile Asn Glu Arg Pro Ala Leu Asp  
 515 520 525

Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu Ser Pro Asp Thr Arg Ala  
 530 535 540

Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu Gln Arg Asn Ile Gly Leu  
 545 550 555 560

Glu Ile Lys Asp Val Gln Ile Ile Lys Gln Ser Glu Lys Glu Tyr Ile  
 565 570 575

Arg Ile Asp Ala Lys Val Val Pro Lys Ser Lys Ile Asp Thr Lys Ile  
 580 585 590

Gln Glu Ala Gln Leu Asn Ile Asn Gln Glu Trp Asn Lys Ala Leu Gly  
 595 600 605

Leu Pro Lys Tyr Thr Lys Leu Ile Thr Phe Asn Val His Asn Arg Tyr  
 610 615 620

Ala Ser Asn Ile Val Glu Ser Ala Tyr Leu Ile Leu Asn Glu Trp Lys  
 625 630 635 640

Asn Asn Ile Gln Ser Asp Leu Ile Lys Lys Val Thr Asn Tyr Leu Val  
 645 650 655

Asp Gly Asn Gly Arg Phe Val Phe Thr Asp Ile Thr Leu Pro Asn Ile  
 660 665 670

Ala Glu Gln Tyr Thr His Gln Asp Glu Ile Tyr Glu Gln Val His Ser  
 675 680 685

Lys Gly Leu Tyr Val Pro Glu Ser Arg Ser Ile Leu Leu His Gly Pro  
 690 695 700

Ser Lys Gly Val Glu Leu Arg Asn Asp Ser Glu Gly Phe Ile His Glu  
 705 710 715 720

Phe Gly His Ala Val Asp Asp Tyr Ala Gly Tyr Leu Leu Asp Lys Asn  
 725 730 735

Gln Ser Asp Leu Val Thr Asn Ser Lys Lys Phe Ile Asp Ile Phe Lys  
 740 745 750

Glu Glu Gly Ser Asn Leu Thr Ser Tyr Gly Arg Thr Asn Glu Ala Glu  
 755 760 765

Phe Phe Ala Glu Ala Phe Arg Leu Met His Ser Thr Asp His Ala Glu  
 770 775 780

Arg Leu Lys Val Gln Lys Asn Ala Pro Lys Thr Phe Gln Phe Ile Asn  
 785 790 795 800

Asp Gln Ile Lys Phe Ile Ile Asn Ser  
 805

<210> 3  
 <211> 2295  
 <212> DNA  
 <213> *Bacillus anthracis*

<220>  
 <221> CDS  
 <222> (1)..(2292)

<400> 3  
 atg aaa aaa cga aaa gtg tta ata cca tta atg gca ttg tct acg ata 48  
 Met Lys Lys Arg Lys Val Leu Ile Pro Leu Met Ala Leu Ser Thr Ile  
 1 5 10 15

tta gtt tca agc aca ggt aat tta gag gtg att cag gca gaa gtt aaa 96  
 Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys  
 20 25 30

cag gag aac cgg tta tta aat gaa tca gaa tca agt tcc cag ggg tta 144  
 Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu  
 35 40 45

cta gga tac tat ttt agt gat ttg aat ttt caa gca ccc atg gtg gtt 192  
 Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val  
 50 55 60

acc tct tct act aca ggg gat tta tct att cct agt tct gag tta gaa 240  
 Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu  
 65 70 75 80

aat att cca tcg gaa aac caa tat ttt caa tct gct att tgg tca gga 288  
 Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly  
 85 90 95

ttt atc aaa gtt aag aag agt gat gaa tat aca ttt gct act tcc gct 336  
 Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala  
 100 105 110

gat aat cat gta aca atg tgg gta gat gac caa gaa gtg att aat aaa 384  
 Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys  
 115 120 125

gct tct aat tct aac aaa atc aga tta gaa aaa gga aga tta tat caa 432  
 Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln  
 130 135 140

ata aaa att caa tat caa cga gaa aat cct act gaa aaa gga ttg gat 480  
 Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp  
 145 150 155 160

ttc aag ttg tac tgg acc gat tct caa aat aaa aaa gaa gtg att tct 528  
 Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser  
 165 170 175

agt gat aac tta caa ttg cca gaa tta aaa caa aaa tct tcg aac tca 576  
 Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser  
 180 185 190



aga aaa aag cga agt aca agt gct gga cct acg gtt cca gac cgt gac	624
Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp	
195 200 205	
aat gat gga atc cct gat tca tta gag gta gaa gga tat acg gtt gat	672
Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp	
210 215 220	
gtc aaa aat aaa aga act ttt ctt tca cca tgg att tct aat att cat	720
Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His	
225 230 235 240	
gaa aag aaa gga tta acc aaa tat aaa tca tct cct gaa aaa tgg agc	768
Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser	
245 250 255	
acg gct tct gat ccg tac agt gat ttc gaa aag gtt aca gga cgg att	816
Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile	
260 265 270	
gat aag aat gta tca cca gag gca aga cac ccc ctt gtg gca gct tat	864
Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr	
275 280 285	
ccg att gta cat gta gat atg gag aat att att ctc tca aaa aat gag	912
Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu	
290 295 300	
gat caa tcc aca cag aat act gat agt caa acg aga aca ata agt aaa	960
Asp Gln Ser Thr Gln Asn Thr Asp Ser Gln Thr Arg Thr Ile Ser Lys	
305 310 315 320	
aat act tct aca agt agg aca cat act agt gaa gta cat gga aat gca	1008
Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala	
325 330 335	
gaa gtg cat gcg tcg ttc ttt gat att ggt ggg agt gta tct gca gga	1056
Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly	
340 345 350	
ttt agt aat tcg aat tca agt acg gtc gca att gat cat tca cta tct	1104
Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser	
355 360 365	
cta gca ggg gaa aga act tgg gct gaa aca atg ggt tta aat acc gct	1152
Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala	
370 375 380	
gat aca gca aga tta aat gcc aat att aga tat gta aat act ggg acg	1200
Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr	
385 390 395 400	
gct cca atc tac aac gtg tta cca acg act tcg tta gtg tta gga aaa	1248
Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys	
405 410 415	

aat caa aca ctc gcg aca att aaa gct aag gaa aac caa tta agt caa Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln 420 425 430	1296
ata ctt gca cct aat aat tat tat cct tct aaa aac ttg gcg cca atc Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile 435 440 445	1344
gca tta aat gca caa gac gat ttc agt tct act cca att aca atg aat Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn 450 455 460	1392
tac aat caa ttt ctt gag tta gaa aaa acg aaa caa tta aga tta gat Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp 465 470 475 480	1440
acg gat caa gta tat ggg aat ata gca aca tac aat ttt gaa aat gga Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly 485 490 495	1488
aga gtg agg gtg gat aca ggc tcg aac tgg agt gaa gtg tta ccg caa Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln 500 505 510	1536
att caa gaa aca act gca cgt atc att ttt aat gga aaa gat tta aat Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn 515 520 525	1584
ctg gta gaa agg cgg ata gcg gcg gtt aat cct agt gat cca tta gaa Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu 530 535 540	1632
acg act aaa ccg gat atg aca tta aaa gaa gcc ctt aaa ata gca ttt Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe 545 550 555 560	1680
gga ttt aac gaa ccg aat gga aac tta caa tat caa ggg aaa gac ata Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile 565 570 575	1728
acc gaa ttt gat ttt aat ttc gat caa caa aca tct caa aat atc aag Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys 580 585 590	1776
aat cag tta gcg gaa tta aac gca acc aac ata tat act gta tta gat Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp 595 600 605	1824
aaa atc aaa tta aat gca aaa atg aat att tta ata aga gat aaa cgt Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg 610 615 620	1872
ttt cat tat gat aga aat aac ata gca gtt ggg gcg gat gag tca gta Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val 625 630 635 640	1920

gtt aag gag gct cat aga gaa gta att aat tcg tca aca gag gga tta 1968  
 Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu  
 645 650 655  
  
 ttg tta aat att gat aag gat ata aga aaa ata tta tca ggt tat att 2016  
 Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile  
 660 665 670  
  
 gta gaa att gaa gat act gaa ggg ctt aaa gaa gtt ata aat gac aga 2064  
 Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg  
 675 680 685  
  
 tat gat atg ttg aat att tct agt tta cgg caa gat gga aaa aca ttt 2112  
 Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe  
 690 695 700  
  
 ata gat ttt aaa aaa tat aat gat aaa tta ccg tta tat ata agt aat 2160  
 Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn  
 705 710 715 720  
  
 ccc aat tat aag gta aat gta tat gct gtt act aaa gaa aac act att 2208  
 Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile  
 725 730 735  
  
 att aat cct agt gag aat ggg gat act agt acc aac ggg atc aag aaa 2256  
 Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys  
 740 745 750  
  
 att tta atc ttt tct aaa aaa ggc tat gag ata gga taa 2295  
 Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly  
 755 760

&lt;210&gt; 4

&lt;211&gt; 764

&lt;212&gt; PRT

&lt;213&gt; Bacillus anthracis

&lt;400&gt; 4

Met Lys Lys Arg Lys Val Leu Ile Pro Leu Met Ala Leu Ser Thr Ile  
 1 5 10 15  
  
 Leu Val Ser Ser Thr Gly Asn Leu Glu Val Ile Gln Ala Glu Val Lys  
 20 25 30  
  
 Gln Glu Asn Arg Leu Leu Asn Glu Ser Glu Ser Ser Ser Gln Gly Leu  
 35 40 45  
  
 Leu Gly Tyr Tyr Phe Ser Asp Leu Asn Phe Gln Ala Pro Met Val Val  
 50 55 60  
  
 Thr Ser Ser Thr Thr Gly Asp Leu Ser Ile Pro Ser Ser Glu Leu Glu  
 65 70 75 80  
  
 Asn Ile Pro Ser Glu Asn Gln Tyr Phe Gln Ser Ala Ile Trp Ser Gly  
 85 90 95

Phe Ile Lys Val Lys Lys Ser Asp Glu Tyr Thr Phe Ala Thr Ser Ala  
 100 105 110  
 Asp Asn His Val Thr Met Trp Val Asp Asp Gln Glu Val Ile Asn Lys  
 115 120 125  
 Ala Ser Asn Ser Asn Lys Ile Arg Leu Glu Lys Gly Arg Leu Tyr Gln  
 130 135 140  
 Ile Lys Ile Gln Tyr Gln Arg Glu Asn Pro Thr Glu Lys Gly Leu Asp  
 145 150 155 160  
 Phe Lys Leu Tyr Trp Thr Asp Ser Gln Asn Lys Lys Glu Val Ile Ser  
 165 170 175  
 Ser Asp Asn Leu Gln Leu Pro Glu Leu Lys Gln Lys Ser Ser Asn Ser  
 180 185 190  
 Arg Lys Lys Arg Ser Thr Ser Ala Gly Pro Thr Val Pro Asp Arg Asp  
 195 200 205  
 Asn Asp Gly Ile Pro Asp Ser Leu Glu Val Glu Gly Tyr Thr Val Asp  
 210 215 220  
 Val Lys Asn Lys Arg Thr Phe Leu Ser Pro Trp Ile Ser Asn Ile His  
 225 230 235 240  
 Glu Lys Lys Gly Leu Thr Lys Tyr Lys Ser Ser Pro Glu Lys Trp Ser  
 245 250 255  
 Thr Ala Ser Asp Pro Tyr Ser Asp Phe Glu Lys Val Thr Gly Arg Ile  
 260 265 270  
 Asp Lys Asn Val Ser Pro Glu Ala Arg His Pro Leu Val Ala Ala Tyr  
 275 280 285  
 Pro Ile Val His Val Asp Met Glu Asn Ile Ile Leu Ser Lys Asn Glu  
 290 295 300  
 Asp Gln Ser Thr Gln Asn Thr Asp Ser Gln Thr Arg Thr Ile Ser Lys  
 305 310 315 320  
 Asn Thr Ser Thr Ser Arg Thr His Thr Ser Glu Val His Gly Asn Ala  
 325 330 335  
 Glu Val His Ala Ser Phe Phe Asp Ile Gly Gly Ser Val Ser Ala Gly  
 340 345 350  
 Phe Ser Asn Ser Asn Ser Ser Thr Val Ala Ile Asp His Ser Leu Ser  
 355 360 365  
 Leu Ala Gly Glu Arg Thr Trp Ala Glu Thr Met Gly Leu Asn Thr Ala  
 370 375 380  
 Asp Thr Ala Arg Leu Asn Ala Asn Ile Arg Tyr Val Asn Thr Gly Thr  
 385 390 395 400

Ala Pro Ile Tyr Asn Val Leu Pro Thr Thr Ser Leu Val Leu Gly Lys  
405 410 415

Asn Gln Thr Leu Ala Thr Ile Lys Ala Lys Glu Asn Gln Leu Ser Gln  
420 425 430

Ile Leu Ala Pro Asn Asn Tyr Tyr Pro Ser Lys Asn Leu Ala Pro Ile  
435 440 445

Ala Leu Asn Ala Gln Asp Asp Phe Ser Ser Thr Pro Ile Thr Met Asn  
450 455 460

Tyr Asn Gln Phe Leu Glu Leu Glu Lys Thr Lys Gln Leu Arg Leu Asp  
465 470 475 480

Thr Asp Gln Val Tyr Gly Asn Ile Ala Thr Tyr Asn Phe Glu Asn Gly  
485 490 495

Arg Val Arg Val Asp Thr Gly Ser Asn Trp Ser Glu Val Leu Pro Gln  
500 505 510

Ile Gln Glu Thr Thr Ala Arg Ile Ile Phe Asn Gly Lys Asp Leu Asn  
515 520 525

Leu Val Glu Arg Arg Ile Ala Ala Val Asn Pro Ser Asp Pro Leu Glu  
530 535 540

Thr Thr Lys Pro Asp Met Thr Leu Lys Glu Ala Leu Lys Ile Ala Phe  
545 550 555 560

Gly Phe Asn Glu Pro Asn Gly Asn Leu Gln Tyr Gln Gly Lys Asp Ile  
565 570 575

Thr Glu Phe Asp Phe Asn Phe Asp Gln Gln Thr Ser Gln Asn Ile Lys  
580 585 590

Asn Gln Leu Ala Glu Leu Asn Ala Thr Asn Ile Tyr Thr Val Leu Asp  
595 600 605

Lys Ile Lys Leu Asn Ala Lys Met Asn Ile Leu Ile Arg Asp Lys Arg  
610 615 620

Phe His Tyr Asp Arg Asn Asn Ile Ala Val Gly Ala Asp Glu Ser Val  
625 630 635 640

Val Lys Glu Ala His Arg Glu Val Ile Asn Ser Ser Thr Glu Gly Leu  
645 650 655

Leu Leu Asn Ile Asp Lys Asp Ile Arg Lys Ile Leu Ser Gly Tyr Ile  
660 665 670

Val Glu Ile Glu Asp Thr Glu Gly Leu Lys Glu Val Ile Asn Asp Arg  
675 680 685

Tyr Asp Met Leu Asn Ile Ser Ser Leu Arg Gln Asp Gly Lys Thr Phe  
690 695 700

Ile Asp Phe Lys Lys Tyr Asn Asp Lys Leu Pro Leu Tyr Ile Ser Asn  
705 710 715 720

Pro Asn Tyr Lys Val Asn Val Tyr Ala Val Thr Lys Glu Asn Thr Ile  
725 730 735

Ile Asn Pro Ser Glu Asn Gly Asp Thr Ser Thr Asn Gly Ile Lys Lys  
740 745 750

Ile Leu Ile Phe Ser Lys Lys Gly Tyr Glu Ile Gly  
755 760

<210> 5

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
primer

<400> 5

ctgaaaccat cacgtaaaa

19

<210> 6

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
primer

<400> 6

agatctgata tctaaataaa gaacga

26

<210> 7

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
primer

<400> 7

ctcgagacca tgggtt

15

<210> 8

<211> 15

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Synthetic primer

&lt;400&gt; 8

agatcttaat ggaat

15

&lt;210&gt; 9

&lt;211&gt; 2430

&lt;212&gt; DNA

&lt;213&gt; Bacillus anthracis

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(2427)

&lt;400&gt; 9

atg	aat	ata	aaa	aaa	gaa	ttt	ata	aaa	gta	att	agt	atg	tca	tgt	tta	48
Met	Asn	Ile	Lys	Lys	Glu	Phe	Ile	Lys	Val	Ile	Ser	Met	Ser	Cys	Leu	
1				5					10					15		

gta	aca	gca	att	act	ttg	agt	ggt	ccc	gtc	ttt	atc	ccc	ctt	gta	cag	96
Val	Thr	Ala	Ile	Thr	Leu	Ser	Gly	Pro	Val	Phe	Ile	Pro	Leu	Val	Gln	
			20					25					30			

ggg	gcg	ggc	ggt	cat	ggt	gat	gta	ggt	atg	cac	gta	aaa	gag	aaa	gag	144
Gly	Ala	Gly	Gly	His	Gly	Asp	Val	Gly	Met	His	Val	Lys	Glu	Lys	Glu	
		35					40					45				

aaa	aat	aaa	gat	gag	aat	aag	aga	aaa	gat	gaa	gaa	cga	aat	aaa	aca	192
Lys	Asn	Lys	Asp	Glu	Asn	Lys	Arg	Lys	Asp	Glu	Glu	Arg	Asn	Lys	Thr	
	50					55						60				

cag	gaa	gag	cat	tta	aag	gaa	atc	atg	aaa	cac	att	gta	aaa	ata	gaa	240
Gln	Glu	Glu	His	Leu	Lys	Glu	Ile	Met	Lys	His	Ile	Val	Lys	Ile	Glu	
65					70				75					80		

gta	aaa	ggg	gag	gaa	gct	gtt	aaa	aaa	gag	gca	gca	gaa	aag	cta	ctt	288
Val	Lys	Gly	Glu	Glu	Ala	Val	Lys	Lys	Glu	Ala	Ala	Glu	Lys	Leu	Leu	
				85					90					95		

gag	aaa	gta	cca	tct	gat	gtt	tta	gag	atg	tat	aaa	gca	att	gga	gga	336
Glu	Lys	Val	Pro	Ser	Asp	Val	Leu	Glu	Met	Tyr	Lys	Ala	Ile	Gly	Gly	
			100					105					110			

aag	ata	tat	att	gtg	gat	ggt	gat	att	aca	aaa	cat	ata	tct	tta	gaa	384
Lys	Ile	Tyr	Ile	Val	Asp	Gly	Asp	Ile	Thr	Lys	His	Ile	Ser	Leu	Glu	
		115					120					125				

gca	tta	tct	gaa	gat	aag	aaa	aaa	ata	aaa	gac	att	tat	ggg	aaa	gat	432
Ala	Leu	Ser	Glu	Asp	Lys	Lys	Lys	Ile	Lys	Asp	Ile	Tyr	Gly	Lys	Asp	
	130					135					140					

gct	tta	tta	cat	gaa	cat	tat	gta	tat	gca	aaa	gaa	gga	tat	gaa	ccc	480
Ala	Leu	Leu	His	Glu	His	Tyr	Val	Tyr	Ala	Lys	Glu	Gly	Tyr	Glu	Pro	
145					150					155				160		

gta ctt gta atc caa tct tct gaa gat tgt gta gaa aat act gaa aag	528
Val Leu Val Ile Gln Ser Ser Glu Asp Cys Val Glu Asn Thr Glu Lys	
165 170 175	
gca ctg aac gtt tat tat gaa ata ggt aag ata tta tca agg gat att	576
Ala Leu Asn Val Tyr Tyr Glu Ile Gly Lys Ile Leu Ser Arg Asp Ile	
180 185 190	
tta agt aaa att aat caa cca tat cag aaa ttt tta gat gta tta aat	624
Leu Ser Lys Ile Asn Gln Pro Tyr Gln Lys Phe Leu Asp Val Leu Asn	
195 200 205	
acc att aaa aat gca tct gat tca gat gga caa gat ctt tta ttt act	672
Thr Ile Lys Asn Ala Ser Asp Ser Asp Gly Gln Asp Leu Leu Phe Thr	
210 215 220	
aat cag ctt aag gaa cat ccc aca gac ttt tct gta gaa ttc ttg gaa	720
Asn Gln Leu Lys Glu His Pro Thr Asp Phe Ser Val Glu Phe Leu Glu	
225 230 235 240	
caa aat agc aat gag gta caa gaa gta ttt gcg aaa gct ttt gca tat	768
Gln Asn Ser Asn Glu Val Gln Glu Val Phe Ala Lys Ala Phe Ala Tyr	
245 250 255	
tat atc gag cca cag cat cgt gat gtt tta cag ctt tat gca ccg gaa	816
Tyr Ile Glu Pro Gln His Arg Asp Val Leu Gln Leu Tyr Ala Pro Glu	
260 265 270	
gct ttt aat tac atg gat aaa ttt aac gaa caa gaa ata aat cta tcc	864
Ala Phe Asn Tyr Met Asp Lys Phe Asn Glu Gln Glu Ile Asn Leu Ser	
275 280 285	
ttg gaa gaa ctt aaa gat caa cgg atg ctg tca aga tat gaa aaa tgg	912
Leu Glu Glu Leu Lys Asp Gln Arg Met Leu Ser Arg Tyr Glu Lys Trp	
290 295 300	
gaa aag ata aaa cag cac tat caa cac tgg agc gat tct tta tct gaa	960
Glu Lys Ile Lys Gln His Tyr Gln His Trp Ser Asp Ser Leu Ser Glu	
305 310 315 320	
gaa gga aga gga ctt tta aaa aag ctg cag att cct att gag cca aag	1008
Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln Ile Pro Ile Glu Pro Lys	
325 330 335	
aaa gat gac ata att cat tct tta tct caa gaa gaa aaa gag ctt cta	1056
Lys Asp Asp Ile Ile His Ser Leu Ser Gln Glu Glu Lys Glu Leu Leu	
340 345 350	
aaa aga ata caa att gat agt agt gat ttt tta tct act gag gaa aaa	1104
Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe Leu Ser Thr Glu Glu Lys	
355 360 365	
gag ttt tta aaa aag cta caa att gat att cgt gat tct tta tct gaa	1152
Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile Arg Asp Ser Leu Ser Glu	
370 375 380	



gaa gaa aaa gag ctt tta aat aga ata cag gtg gat agt agt aat cct Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln Val Asp Ser Ser Asn Pro 385 390 395 400	1200
tta tct gaa aaa gaa aaa gag ttt tta aaa aag ctg aaa ctt gat att Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys Lys Leu Lys Leu Asp Ile 405 410 415	1248
caa cca tat gat att aat caa agg ttg caa gat aca gga ggg tta att Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln Asp Thr Gly Gly Leu Ile 420 425 430	1296
gat agt ccg tca att aat ctt gat gta aga aag cag tat aaa agg gat Asp Ser Pro Ser Ile Asn Leu Asp Val Arg Lys Gln Tyr Lys Arg Asp 435 440 445	1344
att caa aat att gat gct tta tta cat caa tcc att gga agt acc ttg Ile Gln Asn Ile Asp Ala Leu Leu His Gln Ser Ile Gly Ser Thr Leu 450 455 460	1392
tac aat aaa att tat ttg tat gaa aat atg aat atc aat aac ctt aca Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met Asn Ile Asn Asn Leu Thr 465 470 475 480	1440
gca acc cta ggt gcg gat tta gtt gat tcc act gat aat act aaa att Ala Thr Leu Gly Ala Asp Leu Val Asp Ser Thr Asp Asn Thr Lys Ile 485 490 495	1488
aat aga ggt att ttc aat gaa ttc aaa aaa aat ttc aaa tat agt att Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys Asn Phe Lys Tyr Ser Ile 500 505 510	1536
tct agt aac tat atg att gtt gat ata aat gaa agg cct gca tta gat Ser Ser Asn Tyr Met Ile Val Asp Ile Asn Glu Arg Pro Ala Leu Asp 515 520 525	1584
aat gag cgt ttg aaa tgg aga atc caa tta tca cca gat act cga gca Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu Ser Pro Asp Thr Arg Ala 530 535 540	1632
gga tat tta gaa aat gga aag ctt ata tta caa aga aac atc ggt ctg Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu Gln Arg Asn Ile Gly Leu 545 550 555 560	1680
gaa ata aag gat gta caa ata att aag caa tcc gaa aaa gaa tat ata Glu Ile Lys Asp Val Gln Ile Ile Lys Gln Ser Glu Lys Glu Tyr Ile 565 570 575	1728
agg att gat gcg aaa gta gtg cca aag agt aaa ata gat aca aaa att Arg Ile Asp Ala Lys Val Val Pro Lys Ser Lys Ile Asp Thr Lys Ile 580 585 590	1776
caa gaa gca cag tta aat ata aat cag gaa tgg aat aaa gca tta ggg Gln Glu Ala Gln Leu Asn Ile Asn Gln Glu Trp Asn Lys Ala Leu Gly 595 600 605	1824

tta cca aaa tat aca aag ctt att aca ttc aac gtg cat aat aga tat	1872
Leu Pro Lys Tyr Thr Lys Leu Ile Thr Phe Asn Val His Asn Arg Tyr	
610 615 620	
gca tcc aat att gta gaa agt gct tat tta ata ttg aat gaa tgg aaa	1920
Ala Ser Asn Ile Val Glu Ser Ala Tyr Leu Ile Leu Asn Glu Trp Lys	
625 630 635 640	
aat aat att caa agt gat ctt ata aaa aag gta aca aat tac tta gtt	1968
Asn Asn Ile Gln Ser Asp Leu Ile Lys Lys Val Thr Asn Tyr Leu Val	
645 650 655	
gat ggt aat gga aga ttt gtt ttt acc gat att act ctc cct aat ata	2016
Asp Gly Asn Gly Arg Phe Val Phe Thr Asp Ile Thr Leu Pro Asn Ile	
660 665 670	
gct gaa caa tat aca cat caa gat gag ata tat gag caa gtt cat tca	2064
Ala Glu Gln Tyr Thr His Gln Asp Glu Ile Tyr Glu Gln Val His Ser	
675 680 685	
aaa ggg tta tat gtt cca gaa tcc cgt tct ata tta ctc cat gga cct	2112
Lys Gly Leu Tyr Val Pro Glu Ser Arg Ser Ile Leu Leu His Gly Pro	
690 695 700	
tca aaa ggt gta gaa tta agg aat gat agt gag ggt ttt ata cac gaa	2160
Ser Lys Gly Val Glu Leu Arg Asn Asp Ser Glu Gly Phe Ile His Glu	
705 710 715 720	
ttt gga cat gct gtg gat gat tat gct gga tat cta tta gat aag aac	2208
Phe Gly His Ala Val Asp Asp Tyr Ala Gly Tyr Leu Leu Asp Lys Asn	
725 730 735	
caa tct gat tta gtt aca aat tct aaa aaa ttc att gat att ttt aag	2256
Gln Ser Asp Leu Val Thr Asn Ser Lys Lys Phe Ile Asp Ile Phe Lys	
740 745 750	
gaa gaa ggg agt aat tta act tcg tat ggg aga aca aat gaa gcg gaa	2304
Glu Glu Gly Ser Asn Leu Thr Ser Tyr Gly Arg Thr Asn Glu Ala Glu	
755 760 765	
ttt ttt gca gaa gcc ttt agg tta atg cat tct acg gac cat gct gaa	2352
Phe Phe Ala Glu Ala Phe Arg Leu Met His Ser Thr Asp His Ala Glu	
770 775 780	
cgt tta aaa gtt caa aaa aat gct ccg aaa act ttc caa ttt att aac	2400
Arg Leu Lys Val Gln Lys Asn Ala Pro Lys Thr Phe Gln Phe Ile Asn	
785 790 795 800	
gat cag att aag ttc att att aac tca taa	2430
Asp Gln Ile Lys Phe Ile Ile Asn Ser	
805	

&lt;210&gt; 10

&lt;211&gt; 809

&lt;212&gt; PRT

&lt;213&gt; Bacillus anthracis

&lt;400&gt; 10

Met	Asn	Ile	Lys	Lys	Glu	Phe	Ile	Lys	Val	Ile	Ser	Met	Ser	Cys	Leu
1				5					10					15	
Val	Thr	Ala	Ile	Thr	Leu	Ser	Gly	Pro	Val	Phe	Ile	Pro	Leu	Val	Gln
			20					25					30		
Gly	Ala	Gly	Gly	His	Gly	Asp	Val	Gly	Met	His	Val	Lys	Glu	Lys	Glu
		35					40					45			
Lys	Asn	Lys	Asp	Glu	Asn	Lys	Arg	Lys	Asp	Glu	Glu	Arg	Asn	Lys	Thr
	50					55					60				
Gln	Glu	Glu	His	Leu	Lys	Glu	Ile	Met	Lys	His	Ile	Val	Lys	Ile	Glu
65					70					75					80
Val	Lys	Gly	Glu	Glu	Ala	Val	Lys	Lys	Glu	Ala	Ala	Glu	Lys	Leu	Leu
				85					90					95	
Glu	Lys	Val	Pro	Ser	Asp	Val	Leu	Glu	Met	Tyr	Lys	Ala	Ile	Gly	Gly
			100					105						110	
Lys	Ile	Tyr	Ile	Val	Asp	Gly	Asp	Ile	Thr	Lys	His	Ile	Ser	Leu	Glu
		115					120						125		
Ala	Leu	Ser	Glu	Asp	Lys	Lys	Lys	Ile	Lys	Asp	Ile	Tyr	Gly	Lys	Asp
	130					135						140			
Ala	Leu	Leu	His	Glu	His	Tyr	Val	Tyr	Ala	Lys	Glu	Gly	Tyr	Glu	Pro
145					150					155					160
Val	Leu	Val	Ile	Gln	Ser	Ser	Glu	Asp	Cys	Val	Glu	Asn	Thr	Glu	Lys
				165					170					175	
Ala	Leu	Asn	Val	Tyr	Tyr	Glu	Ile	Gly	Lys	Ile	Leu	Ser	Arg	Asp	Ile
			180					185					190		
Leu	Ser	Lys	Ile	Asn	Gln	Pro	Tyr	Gln	Lys	Phe	Leu	Asp	Val	Leu	Asn
		195					200					205			
Thr	Ile	Lys	Asn	Ala	Ser	Asp	Ser	Asp	Gly	Gln	Asp	Leu	Leu	Phe	Thr
	210					215					220				
Asn	Gln	Leu	Lys	Glu	His	Pro	Thr	Asp	Phe	Ser	Val	Glu	Phe	Leu	Glu
225					230					235					240
Gln	Asn	Ser	Asn	Glu	Val	Gln	Glu	Val	Phe	Ala	Lys	Ala	Phe	Ala	Tyr
				245					250					255	
Tyr	Ile	Glu	Pro	Gln	His	Arg	Asp	Val	Leu	Gln	Leu	Tyr	Ala	Pro	Glu
			260					265					270		
Ala	Phe	Asn	Tyr	Met	Asp	Lys	Phe	Asn	Glu	Gln	Glu	Ile	Asn	Leu	Ser
		275					280					285			
Leu	Glu	Glu	Leu	Lys	Asp	Gln	Arg	Met	Leu	Ser	Arg	Tyr	Glu	Lys	Trp
	290					295					300				

Glu Lys Ile Lys Gln His Tyr Gln His Trp Ser Asp Ser Leu Ser Glu  
 305 310 315 320  
 Glu Gly Arg Gly Leu Leu Lys Lys Leu Gln Ile Pro Ile Glu Pro Lys  
 325 330 335  
 Lys Asp Asp Ile Ile His Ser Leu Ser Gln Glu Glu Lys Glu Leu Leu  
 340 345 350  
 Lys Arg Ile Gln Ile Asp Ser Ser Asp Phe Leu Ser Thr Glu Glu Lys  
 355 360 365  
 Glu Phe Leu Lys Lys Leu Gln Ile Asp Ile Arg Asp Ser Leu Ser Glu  
 370 375 380  
 Glu Glu Lys Glu Leu Leu Asn Arg Ile Gln Val Asp Ser Ser Asn Pro  
 385 390 395 400  
 Leu Ser Glu Lys Glu Lys Glu Phe Leu Lys Lys Leu Lys Leu Asp Ile  
 405 410 415  
 Gln Pro Tyr Asp Ile Asn Gln Arg Leu Gln Asp Thr Gly Gly Leu Ile  
 420 425 430  
 Asp Ser Pro Ser Ile Asn Leu Asp Val Arg Lys Gln Tyr Lys Arg Asp  
 435 440 445  
 Ile Gln Asn Ile Asp Ala Leu Leu His Gln Ser Ile Gly Ser Thr Leu  
 450 455 460  
 Tyr Asn Lys Ile Tyr Leu Tyr Glu Asn Met Asn Ile Asn Asn Leu Thr  
 465 470 475 480  
 Ala Thr Leu Gly Ala Asp Leu Val Asp Ser Thr Asp Asn Thr Lys Ile  
 485 490 495  
 Asn Arg Gly Ile Phe Asn Glu Phe Lys Lys Asn Phe Lys Tyr Ser Ile  
 500 505 510  
 Ser Ser Asn Tyr Met Ile Val Asp Ile Asn Glu Arg Pro Ala Leu Asp  
 515 520 525  
 Asn Glu Arg Leu Lys Trp Arg Ile Gln Leu Ser Pro Asp Thr Arg Ala  
 530 535 540  
 Gly Tyr Leu Glu Asn Gly Lys Leu Ile Leu Gln Arg Asn Ile Gly Leu  
 545 550 555 560  
 Glu Ile Lys Asp Val Gln Ile Ile Lys Gln Ser Glu Lys Glu Tyr Ile  
 565 570 575  
 Arg Ile Asp Ala Lys Val Val Pro Lys Ser Lys Ile Asp Thr Lys Ile  
 580 585 590  
 Gln Glu Ala Gln Leu Asn Ile Asn Gln Glu Trp Asn Lys Ala Leu Gly  
 595 600 605

Leu Pro Lys Tyr Thr Lys Leu Ile Thr Phe Asn Val His Asn Arg Tyr  
 610 615 620  
 Ala Ser Asn Ile Val Glu Ser Ala Tyr Leu Ile Leu Asn Glu Trp Lys  
 625 630 635 640  
 Asn Asn Ile Gln Ser Asp Leu Ile Lys Lys Val Thr Asn Tyr Leu Val  
 645 650 655  
 Asp Gly Asn Gly Arg Phe Val Phe Thr Asp Ile Thr Leu Pro Asn Ile  
 660 665 670  
 Ala Glu Gln Tyr Thr His Gln Asp Glu Ile Tyr Glu Gln Val His Ser  
 675 680 685  
 Lys Gly Leu Tyr Val Pro Glu Ser Arg Ser Ile Leu Leu His Gly Pro  
 690 695 700  
 Ser Lys Gly Val Glu Leu Arg Asn Asp Ser Glu Gly Phe Ile His Glu  
 705 710 715 720  
 Phe Gly His Ala Val Asp Asp Tyr Ala Gly Tyr Leu Leu Asp Lys Asn  
 725 730 735  
 Gln Ser Asp Leu Val Thr Asn Ser Lys Lys Phe Ile Asp Ile Phe Lys  
 740 745 750  
 Glu Glu Gly Ser Asn Leu Thr Ser Tyr Gly Arg Thr Asn Glu Ala Glu  
 755 760 765  
 Phe Phe Ala Glu Ala Phe Arg Leu Met His Ser Thr Asp His Ala Glu  
 770 775 780  
 Arg Leu Lys Val Gln Lys Asn Ala Pro Lys Thr Phe Gln Phe Ile Asn  
 785 790 795 800  
 Asp Gln Ile Lys Phe Ile Ile Asn Ser  
 805